SEQUENCE LISTING

<110> Meyers, Rachel A.

<120> 33521, A NOVEL HUMAN GUANINE NUCLEOTIDE EXCHANGE FAMILY MEMBER AND USES THEREOF

<130> 10448-095001

<150> 60/235,033

<151> 2000-09-25

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5437

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (248)...(5350)

<400> 1

	20
ggatacette agecagetea ttetggatga atgaatgatt acactaagtg teetecacat 1	
tootetgtgg geteacttea tggacteact ttgegtgett gttaaatgtg etgegttget 19	80
cccaagacca tgtaaagcct actgaccact aacctccctc acagcagaaa ctagacgtca 24	40
ggttaaa atg ggc aac tcc gac agt cag tac acc ctt caa gga tct aaa 2	89
Met Gly Asn Ser Asp Ser Gln Tyr Thr Leu Gln Gly Ser Lys	
1 5 10	
	37
Asn His Ser Asn Thr Ile Thr Gly Ala Lys Gln Ile Pro Cys Ser Leu 15 20 25 30	
25 25 30	

aaa ata cgt ggc gtt cat gca aaa gag gaa aag tca ttg cat gga tgg
Lys Ile Arg Gly Val His Ala Lys Glu Glu Lys Ser Leu His Gly Trp
35 40 45

ggt cac ggg agc aac gga gca ggt tac aag tcc agg tcc ctg gcc cga 433 Gly His Gly Ser Asn Gly Ala Gly Tyr Lys Ser Arg Ser Leu Ala Arg 50 55 60

agc tgc ctt tct cac ttt aag agt aac cag cct tac gca tcg aga ctc

Ser Cys Leu Ser His Phe Lys Ser Asn Gln Pro Tyr Ala Ser Arg Leu

65

70

75

ggt ggc ccc aca tgc aag gtc tcc aga ggt gtt gcc tac tcc acg cac 529 Gly Gly Pro Thr Cys Lys Val Ser Arg Gly Val Ala Tyr Ser Thr His 80 85 90

agg aca aat gcc cca ggg aag gat ttc cag ggc atc agt gct gct ttc 577

7\ ~~ ~	mh w	7.00	71 -	Dwo	C1	Tvo	Λαn	Phe	Cln	Clu	Tlo	Sor	ЛΊэ	בות	Dhe	
95	IIIT	ASII	Ald	PIO	100	пÃ2	ASP	rne	GIII	105	116	261	ALG	AIG	110	
								gtt Val								625
								gga Gly 135								673
								cca Pro								721
								ggg Gly								769
								ccc Pro								817
								agg Arg								865
								agg Arg 215								913
								acg Thr								961
								tca Ser								1009
ggc Gly 255	aat Asn	gct Ala	gga Gly	gag Glu	ctg Leu 260	agc Ser	gag Glu	gct Ala	gag Glu	ggc Gly 265	tcc Ser	ttc Phe	ctg Leu	gcc Ala	ccc Pro 270	1057
ggc	atg Met	cct Pro	gac Asp	ccc Pro 275	agt Ser	ctc Leu	cat His	gcc Ala	agc Ser 280	ttc Phe	cca Pro	cct Pro	ggc Gly	gat Asp 285	gcc Ala	1105
aaa Lys	aag Lys	cct Pro	ttc Phe 290	aac Asn	caa Gln	agc Ser	tct Ser	tcc Ser 295	ctc Leu	tcc Ser	tcc Ser	ctc Leu	cgg Arg 300	Glu	ctg Leu	1153
tac Tyr	aaa Lys	gat Asp 305	Ala	aac Asn	ctg Leu	ggg	agc Ser 310		tcc Ser	ccc Pro	tca Ser	ggt Gly 315	Ile	cgc Arg	ctt Leu	1201
tct Ser	gat Asp	gaa Glu	tac Tyr	atg Met	ggc Gly	acg Thr	cat His	gcc Ala	agc Ser	ctg Leu	ago Ser	aac Asn	cgt Arg	gtc Val	tct	1249

	320					325				330				
	gct Ala													1297
	cag Gln		_					_		_		-		1345
	gag Glu													1393
	agt Ser	_		_		_			_				_	1441
	ccg Pro 400													1489
	ctg Leu													1537
	tca Ser													1585
	gcg Ala			_	-			_						1633
-	cga Arg		-	-	_	_						_		1681
	aca Thr 480													1729
	ctg Leu													1777
	tgg Trp													1825
	gag Glu													1873
	gga Gly													1921

gat Asp	cag Gln 560	agc Ser	agt Ser	gcc Ala	cct Pro	cgg Arg 565	tgt Cys	gct Ala	ctg Leu	ttt Phe	gca Ala 570	gaa Glu	gac Asp	agc Ser	ata Ile	1969
gtg Val 575	cag Gln	tct Ser	gtt Val	cca Pro	gag Glu 580	cat His	ccc Pro	aag Lys	aaa Lys	gaa Glu 585	aat Asn	gtg Val	ttc Phe	tgc Cys	ctc Leu 590	2017
agc Ser	aac Asn	tcc Ser	ttt Phe	gga Gly 595	gat Asp	gtc Val	tac Tyr	ctt Leu	ttc Phe 600	cag Gln	gcc Ala	acc Thr	agc Ser	cag Gln 605	aca Thr	2065
gat Asp	cta Leu	gaa Glu	aac Asn 610	tgg Trp	gtc Val	act Thr	gct Ala	gta Val 615	cac His	tct Ser	gct Ala	tgt Cys	gca Ala 620	tcc Ser	ctt Leu	2113
ttt Phe	gca Ala	aag Lys 625	aag Lys	cat His	ggg	aaa Lys	gag Glu 630	gac Asp	acg Thr	ctg Leu	cgg Arg	ctg Leu 635	ctg Leu	aag Lys	aac Asn	2161
cag Gln	acc Thr 640	aaa Lys	aac Asn	ctg Leu	ctt Leu	cag Gln 645	aag Lys	ata Ile	gac Asp	atg Met	gac Asp 650	agc Ser	aag Lys	atg Met	aag Lys	2209
aag Lys 655	atg Met	gca Ala	gag Glu	ctg Leu	cag Gln 660	ctg Leu	tcc Ser	gtg Val	gtg Val	agc Ser 665	gac Asp	cca Pro	aag Lys	aac Asn	agg Arg 670	2257
aaa Lys	gcc Ala	ata Ile	gag Glu	aac Asn 675	cag Gln	atc Ile	cag Gln	caa Gln	tgg Trp 680	gag Glu	cag Gln	aat Asn	ctt Leu	gag Glu 685	aaa Lys	2305
ttt Phe	cac His	atg Met	gat Asp 690	Leu	ttc Phe	agg Arg	atg Met	cgc Arg 695	tgc Cys	tat Tyr	ctg Leu	gcc Ala	agc Ser 700	Leu	caa Gln	2353
ggt Gly	ggg	gag Glu 705	Leu	ccg Pro	aac Asn	cca Pro	aag Lys 710	Ser	ctc Leu	ctt Leu	gca Ala	gcc Ala 715	Ala	agc Ser	cgc Arg	2401
ccc Pro	tcc Ser 720	Lys	ctg Leu	gcc Ala	ctc Leu	ggc Gly 725	Arg	ctg Leu	ggc	ato Ile	ttg Leu 730	Ser	gtt Val	tcc Ser	tct Ser	2449
tto Phe 735	His	gct Ala	. ctg . Leu	gta Val	tgt Cys 740	Ser	aga Arg	gat JAsp	gac Asp	tct Ser 745	Ala	cto Leu	cgg Arg	ı aaa ı Lys	agg Arg 750	2497
aca Thr	ctç Lev	g tca Ser	cto Lev	acc Thr 755	Glr	g cga Arg	dgg Gl	g aga / Arc	aac Asr 760	ı Lys	g aag S Lys	g gga s Gly	ata / Ile	ttte Phe	tct Ser	2545
tco Ser	g tta Lei	a aaa 1 Lys	ggg Gly	/ Lei	g gad 1 Asp	c aca	t Cto	g gco ı Ala 775	a Arg	a aaa g Lys	a ggo s Gly	c aaq y Lys	g gaç s Glu 780	ı Lys	g aga s Arg	2593

	F	# #	
i	į	H. H. H. H.	
;	ŧ	Į	
١	Ĺ	ř	
•		ā,	
;	į		
:		# 12	
		2	2
:	ŧ	7	
;	3		
;	3		
	E 0E	# # # # #	The same of
	TH GE .4 7	H H HH stude	Terrait Thomas I
	TH GE .4 7	H H HH stude	Terrait Thomas I
	TH GE .4 7	# # # # #	Terrait Thomas I

				cag Gln												2641	
				ccc Pro												2689	
				aat Asn												2737	
				att Ile 835												2785	
ccc Pro	agc Ser	cat His	tat Tyr 850	ggc Gly	cta Leu	cag Gln	ctt Leu	cga Arg 855	aaa Lys	tta Leu	gta Val	gat Asp	gac Asp 860	aat Asn	gtt Val	2833	
gag Glu	tat Tyr	tgc Cys 865	atc Ile	cct Pro	gca Ala	cca Pro	tat Tyr 870	gaa Glu	tat Tyr	atg Met	caa Gln	caa Gln 875	cag Gln	gtt Val	tat Tyr	2881	
gat Asp	gaa Glu 880	ata Ile	gaa Glu	gtc Val	ttt Phe	cca Pro 885	cta Leu	aat Asn	gtt Val	tat Tyr	gat Asp 890	gtg Val	cag Gln	ctc Leu	acg Thr	2929	
aag Lys 895	act Thr	ggg Gly	agt Ser	gtg Val	tgt Cys 900	gac Asp	ttt Phe	ggg Gly	ttt Phe	gca Ala 905	gtt Val	aca Thr	gcg Ala	cag Gln	gtg Val 910	2977	
gat Asp	gag Glu	cgt Arg	cag Gln	cat His 915	ctc Leu	agc Ser	cgg Arg	ata Ile	ttt Phe 920	ata Ile	agc Ser	gac Asp	gtt Val	ctt Leu 925	ccc Pro	3025	
gat Asp	ggc Gly	ctg Leu	gcg Ala 930	tat Tyr	Gly	gaa Glu	ggg	ctg Leu 935	aga Arg	aag Lys	ggc Gly	aat Asn	gag Glu 940	atc Ile	atg Met	3073	
acc Thr	tta Leu	aat Asn 945	Gly	gaa Glu	gct Ala	gtg Val	tct Ser 950	gat Asp	ctt Leu	gac Asp	ctt Leu	aag Lys 955	cag Gln	atg Met	gag Glu	3121	
gcc Ala	ctg Leu 960	Phe	tct Ser	gag Glu	aag Lys	agc Ser 965	gtc Val	gga Gly	ctc Leu	act Thr	ctg Leu 970	Ile	gcc Ala	cgg Arg	cct Pro	3169	
ccg Pro 975	Asp	aca Thr	aaa Lys	gca Ala	acc Thr 980	Leu	tgt Cys	aca Thr	tcc Ser	tgg Trp 985	Ser	gac Asp	agt Ser	gac Asp	ctg Leu 990	3217	
ttc Phe	tcc Ser	agg Arg	gac Asp	cag Gln 99	Lys	agt Ser	ctg Leu	ctg Leu	ccc Pro 100	Pro	cct Pro	aac Asn	cag Gln	tcc Ser 100	caa Gln 5	3265	
ctg	ctg	gag	g gaa	ttc	ctg	gat	aac	ttt	. aaa	aag	, aat	aca	gcc	aat	gat	3313	

I	Leu	Leu	Glu	Glu 1010		Leu	Asp	Asn	Phe 1015		Lys	Asn	Thr	Ala 1020		Asp	
t	tc Phe	agc Ser	aac Asn 1025	Val	cct Pro	gat Asp	atc Ile	aca Thr 1030	Thr	ggt Gly	ctg Leu	aaa Lys	agg Arg 1035	Ser	cag Gln	aca Thr	3361
			Thr					Ser				aaa Lys 1050	Met				3409
]		Arg					Ile					agg Arg					3457
ć	agt Ser	cag Gln	gcc Ala	aac Asn	ggc Gly 1075	Met	gaa Glu	gga Gly	ccg Pro	cgg Arg _. 1080	Glu	aat Asn	cag Gln	gat Asp	cct Pro 1085	Pro	3505
					Ala					Asp		gac Asp			Arg		3553
,	gtc Val	atc Ile	cag Gln 1105	Glu	ctt Leu	gtg Val	gac Asp	aca Thr 111	Glu	aag Lys	tcc Ser	tac Tyr	gtg Val 111	Lys	gat Asp	ttg Leu	3601
į	agc Ser	tgc Cys 1120	Leu	ttt Phe	gaa Glu	tta Leu	tac Tyr 112	Leu	gag Glu	cca Pro	ctt Leu	cag Gln 1130	Asn	gag Glu	acc Thr	ttt Phe	3649
	ctt Leu 113	Thr	caa Gln	gat Asp	gag Glu	atg Met 114	Glu	tca Ser	ctt Leu	ttt Phe	gga Gly 114	agt Ser 5	ttg Leu	cca Pro	gag Glu	atg Met 1150	3697
						Val					Leu	gag Glu				Ser	3745
	gca Ala	tca Ser	tct Ser	gac Asp 117	Phe	aac Asn	acc Thr	cta Leu	gaa Glu 117	Thr	ccc Pro	tca Ser	cag Gln	ttt Phe 118	Arg	aaa Lys	3793
	tta Leu	ctg Leu	ttt Phe 118	Ser	ctt Leu	gga Gly	ggc Gly	tct Ser 119	Phe	ctt Leu	tat Tyr	tac Tyr	gcg Ala 119	Asp	cac His	ttt Phe	3841
	aaa Lys	ctg Leu 120	Tyr	agt Ser	gga Gly	ttc Phe	tgt Cys 120	Ala	aac Asn	cat His	atc Ile	aaa Lys 121	Val	cag Gln	aag Lys	gtt Val	3889
		Glu					Asp					Ala				gcc Ala 1230	3937
																atc	3985

1240 1245 1235 aag ccg gtt cag aga gtg ctc aag tac ccg ctg ctc caag gag ctg 4033 Lys Pro Val Gln Arg Val Leu Lys Tyr Pro Leu Leu Lys Glu Leu 1255 1250 gtg tcc ctg acg gac cag gag agc gag gag cac tac cac ctg acg gaa 4081 Val Ser Leu Thr Asp Gln Glu Ser Glu Glu His Tyr His Leu Thr Glu 1265 1270 4129 qca cta aaq qca atq qag aaa gta gcg agc cac atc aat gag atg cag Ala Leu Lys Ala Met Glu Lys Val Ala Ser His Ile Asn Glu Met Gln 1285 1280 4177 aaq atc tat qaq qat tat ggg acc gtg ttt gac cag cta gta gct gag Lys Ile Tyr Glu Asp Tyr Gly Thr Val Phe Asp Gln Leu Val Ala Glu 1300 1305 1295 4225 cag age qga aca qag aaq qag qta aca gaa ctt teg atg gga gag ett Gln Ser Gly Thr Glu Lys Glu Val Thr Glu Leu Ser Met Gly Glu Leu 1315 ctg atg cac tct acg gtt tcc tgg ttg aat cca ttt ctg tct cta gga 4273 Leu Met His Ser Thr Val Ser Trp Leu Asn Pro Phe Leu Ser Leu Gly 1330 1335 aaa gct aga aag gac ctt gag ctc aca gta ttt gtt ttt aag aga gcc 4321 Lys Ala Arg Lys Asp Leu Glu Leu Thr Val Phe Val Phe Lys Arg Ala 1345 1350 gtc ata ctg gtt tat aaa gaa aac tgc aaa ctg aaa aag aaa ttg ccc 4369 Val Ile Leu Val Tyr Lys Glu Asn Cys Lys Leu Lys Lys Leu Pro 1365 1370 1360 tcg aat tcc cgg cct gca cac aac tct act gac ttg gac cca ttt aaa 4417 Ser Asn Ser Arg Pro Ala His Asn Ser Thr Asp Leu Asp Pro Phe Lys 1385 1390 1380 1375 ttc cgc tgg ttg atc ccc atc tcc gcg ctt caa gtc aga ctg ggg aat 4465 Phe Arg Trp Leu Ile Pro Ile Ser Ala Leu Gln Val Arg Leu Gly Asn 1400 1405 1395 cca gca ggg aca gaa aat aat tcc ata tgg gaa ctg atc cat acg aag 4513 Pro Ala Gly Thr Glu Asn Asn Ser Ile Trp Glu Leu Ile His Thr Lys 1415 1410 tca gaa ata gaa gga cgg cca gaa acc atc ttt cag ttg tgt tgc agt 4561 Ser Glu Ile Glu Gly Arg Pro Glu Thr Ile Phe Gln Leu Cys Cys Ser 1430 1425 gac agt gaa agc aaa acc aac att gtt aag gtg att cgt tct att ctg 4609 Asp Ser Glu Ser Lys Thr Asn Ile Val Lys Val Ile Arg Ser Ile Leu 1445 1440 agg gaa aac ttc agg cgt cac ata aag tgt gaa tta cca ctg gag aaa 4657 Arg Glu Asn Phe Arg Arg His Ile Lys Cys Glu Leu Pro Leu Glu Lys 1455 1460 1465 1470

acg tgt aag gat Thr Cys Lys Asp	cgc ctg gta Arg Leu Val 1475	cct ctt aag aa Pro Leu Lys As 1480	sn Arg Val Pro V	gtt tcg 4705 Val Ser 1485
gcc aaa tta gct Ala Lys Leu Ala 1490	Ser Ser Arg			
agc aac gag tgg Ser Asn Glu Trp 1505	acc ggt gag Thr Gly Glu	act ggc aag gg Thr Gly Lys Gl 1510	ga acc ttg ctg o Ly Thr Leu Leu <i>I</i> 1515	gac tct 4801 Asp Ser
gac gag ggc agc Asp Glu Gly Ser 1520	ttg agc agc Leu Ser Ser 1525	Gly Thr Gln Se	gc agc ggc tgc o er Ser Gly Cys I 1530	ccc acg 4849 Pro Thr
gct gag ggc agg Ala Glu Gly Arg 1535	cag gac tcc Gln Asp Ser 1540	Lys Ser Thr Se	ct ccc ggg aaa t er Pro Gly Lys : 545	tac cca 4897 Tyr Pro 1550
cac ccc ggc ttg His Pro Gly Leu	gca gat ttt Ala Asp Phe 1555	gcc gac aat c Ala Asp Asn L 1560	eu Ile Lys Glu :	agt gac 4945 Ser Asp 1565
atc ctg agc gat Ile Leu Ser Asp 1570	Glu Asp Asp	gac cac cgt c Asp His Arg G 1575	ag act gtg aag o ln Thr Val Lys (1580	cag ggc 4993 Gln Gly
agc cct act aaa Ser Pro Thr Lys 1585	gac atc gaa Asp Ile Glu	att cag ttc c Ile Gln Phe G 1590	ag aga ctg agg ln Arg Leu Arg 1595	att tcc 5041 Ile Ser
gag gac cca gac Glu Asp Pro Asp 1600	gtt cac ccc Val His Pro 160	Glu Ala Glu G	ag cag cct ggc ln Gln Pro Gly 1610	ccg gag 5089 Pro Glu
tcg ggt gag ggt Ser Gly Glu Gly 1615	cag aaa gga Gln Lys Gly 1620	Gly Glu Gln P	cc aaa ctg gtc ro Lys Leu Val 625	cgg ggg 5137 Arg Gly 1630
cac ttc tgc ccc His Phe Cys Pro	att aaa cga Ile Lys Arg 1635	aaa gcc aac a Lys Ala Asn S 1640	er Thr Lys Arg	gac aga 5185 Asp Arg 1645
gga act ttg ctc Gly Thr Leu Leu 165	. Lys Ala Gln	atc cgt cac c Ile Arg His G 1655	ag tcc ctt gac In Ser Leu Asp 1660	Ser Gln
tct gaa aat gcc Ser Glu Asn Ala 1665	acc atc gac Thr Ile Asp	cta aat tct g Leu Asn Ser V 1670	tt cta gag cga Val Leu Glu Arg 1675	gaa ttc 5281 Glu Phe
agt gtc cag agt Ser Val Gln Ser 1680	tta aca tct Leu Thr Ser 168	Val Val Ser G	gag gag tgt ttt Slu Glu Cys Phe 1690	tat gaa 5329 Tyr Glu

5437

aca gag agc cac gga aaa tca tagtatgatt caatccagat atgggttaaa 5380 Thr Glu Ser His Gly Lys Ser 1695 1700

ttcctcattt tacttttaaa ctggtggtaa agtggaaatt gcaaaaaaaa aaaaaaa

<210> 2 <211> 1701

<212> PRT

<213> Homo sapiens

Asn Ala Pro Gly Lys Asp Phe Gln Gly Ile Ser Ala Ala Phe Ser Thr

Glu Asn Gly Phe His Ser Val Gly His Glu Leu Ala Asp Asn His Ile 115 120 125

Thr Ser Arg Asp Cys Asn Gly His Leu Leu Asn Cys Tyr Gly Arg Asn 130 135 140 Glu Ser Ile Ala Ser Thr Pro Pro Gly Glu Asp Arg Lys Ser Pro Arg

145 150 155 160
Val Leu Ile Lys Thr Leu Gly Lys Pro Asp Gly Cys Leu Arg Val Glu

Phe His Asn Gly Gly Asn Pro Ser Lys Val Pro Ala Glu Asp Cys Ser 180 185 190

Glu Pro Val Gln Leu Leu Arg Tyr Ser Pro Thr Leu Ala Ser Glu Thr 195 200 205

Ser Pro Val Pro Glu Ala Arg Arg Gly Ser Ser Ala Asp Ser Leu Pro 210 215 220

Ser His Arg Pro Ser Pro Thr Asp Ser Arg Leu Arg Ser Ser Lys Gly 235 230 235

Ser Ser Leu Ser Ser Glu Ser Ser Trp Tyr Asp Ser Pro Trp Gly Asn 245 250 255

Ala Gly Glu Leu Ser Glu Ala Glu Gly Ser Phe Leu Ala Pro Gly Met 260 265 270

Pro Asp Pro Ser Leu His Ala Ser Phe Pro Pro Gly Asp Ala Lys Lys 275 280 285

Pro Phe Asn Gln Ser Ser Ser Leu Ser Ser Leu Arg Glu Leu Tyr Lys 290 295 300

Asp Ala Asn Leu Gly Ser Leu Ser Pro Ser Gly Ile Arg Leu Ser Asp 305 310 315 320

Glu Tyr Met Gly Thr His Ala Ser Leu Ser Asn Arg Val Ser Phe Ala 325 330 335

Ser Asp Ile Asp Val Pro Ser Arg Val Ala His Gly Asp Pro Ile Gln 340 345 350

Tyr Ser Ser Phe Thr Leu Pro Cys Arg Lys Pro Lys Ala Phe Val Glu

355 360 Asp Thr Ala Lys Lys Asp Ser Leu Lys Ala Arg Met Arg Arg Ile Ser 375 Asp Trp Thr Gly Ser Leu Ser Arg Lys Lys Arg Lys Leu Gln Glu Pro 390 395 Arg Ser Lys Glu Gly Ser Asp Tyr Phe Asp Ser Arg Ser Asp Gly Leu 410 405 Asn Thr Asp Val Gln Gly Ser Ser Gln Ala Ser Ala Phe Leu Trp Ser 420 425 Gly Gly Ser Thr Gln Ile Leu Ser Gln Arg Ser Glu Ser Thr His Ala 440 Ile Gly Ser Asp Pro Leu Arg Gln Asn Ile Tyr Glu Asn Phe Met Arg 455 Glu Leu Glu Met Ser Arg Thr Asn Thr Glu Asn Ile Glu Thr Ser Thr 470 475 Glu Thr Ala Glu Ser Ser Ser Glu Ser Leu Ser Ser Leu Glu Gln Leu 490 485 Asp Leu Leu Phe Glu Lys Glu Gln Gly Val Val Arg Arg Ala Gly Trp Leu Phe Phe Lys Pro Leu Val Thr Val Gln Lys Glu Arg Lys Leu Glu 520 Leu Val Ala Arg Arg Lys Trp Lys Gln Tyr Trp Val Thr Leu Lys Gly 535 Cys Thr Leu Leu Phe Tyr Glu Thr Tyr Gly Lys Asn Ser Met Asp Gln 555 550 Ser Ser Ala Pro Arg Cys Ala Leu Phe Ala Glu Asp Ser Ile Val Gln 565 570 Ser Val Pro Glu His Pro Lys Lys Glu Asn Val Phe Cys Leu Ser Asn 585 580 Ser Phe Gly Asp Val Tyr Leu Phe Gln Ala Thr Ser Gln Thr Asp Leu 600 Glu Asn Trp Val Thr Ala Val His Ser Ala Cys Ala Ser Leu Phe Ala 620 615 Lys Lys His Gly Lys Glu Asp Thr Leu Arg Leu Leu Lys Asn Gln Thr 630 635 Lys Asn Leu Leu Gln Lys Ile Asp Met Asp Ser Lys Met Lys Lys Met 645 650 Ala Glu Leu Gln Leu Ser Val Val Ser Asp Pro Lys Asn Arg Lys Ala 665 660 Ile Glu Asn Gln Ile Gln Gln Trp Glu Gln Asn Leu Glu Lys Phe His 680 Met Asp Leu Phe Arg Met Arg Cys Tyr Leu Ala Ser Leu Gln Gly Gly 695 Glu Leu Pro Asn Pro Lys Ser Leu Leu Ala Ala Ala Ser Arg Pro Ser 710 Lys Leu Ala Leu Gly Arg Leu Gly Ile Leu Ser Val Ser Ser Phe His 730 725 Ala Leu Val Cys Ser Arg Asp Asp Ser Ala Leu Arg Lys Arg Thr Leu 745 Ser Leu Thr Gln Arg Gly Arg Asn Lys Lys Gly Ile Phe Ser Ser Leu 760 Lys Gly Leu Asp Thr Leu Ala Arg Lys Gly Lys Glu Lys Arg Pro Ser 775 780 Ile Thr Gln Val Asp Glu Leu Leu His Ile Tyr Gly Ser Thr Val Asp 790 795 Gly Val Pro Arg Asp Asn Ala Trp Glu Ile Gln Thr Tyr Val His Phe 810 805

Gln Asp Asn His Gly Val Thr Val Gly Ile Lys Pro Glu His Arg Val 825 820 Glu Asp Ile Leu Thr Leu Ala Cys Lys Met Arg Gln Leu Glu Pro Ser 840 845 His Tyr Gly Leu Gln Leu Arg Lys Leu Val Asp Asp Asn Val Glu Tyr 855 Cys Ile Pro Ala Pro Tyr Glu Tyr Met Gln Gln Gln Val Tyr Asp Glu 870 875 Ile Glu Val Phe Pro Leu Asn Val Tyr Asp Val Gln Leu Thr Lys Thr 890 885 Gly Ser Val Cys Asp Phe Gly Phe Ala Val Thr Ala Gln Val Asp Glu 905 Arg Gln His Leu Ser Arg Ile Phe Ile Ser Asp Val Leu Pro Asp Gly 920 Leu Ala Tyr Gly Glu Gly Leu Arg Lys Gly Asn Glu Ile Met Thr Leu 935 Asn Gly Glu Ala Val Ser Asp Leu Asp Leu Lys Gln Met Glu Ala Leu 955 950 Phe Ser Glu Lys Ser Val Gly Leu Thr Leu Ile Ala Arg Pro Pro Asp 970 965 Thr Lys Ala Thr Leu Cys Thr Ser Trp Ser Asp Ser Asp Leu Phe Ser 985 980 Arg Asp Gln Lys Ser Leu Leu Pro Pro Pro Asn Gln Ser Gln Leu Leu 1000 1005 995 Glu Glu Phe Leu Asp Asn Phe Lys Lys Asn Thr Ala Asn Asp Phe Ser 1015 1020 Asn Val Pro Asp Ile Thr Thr Gly Leu Lys Arg Ser Gln Thr Asp Gly 1025 1030 1035 Thr Leu Asp Gln Val Ser His Arg Glu Lys Met Glu Gln Thr Phe Arg 1050 1045 Ser Ala Glu Gln Ile Thr Ala Leu Cys Arg Ser Phe Asn Asp Ser Gln 1070 1060 1065 Ala Asn Gly Met Glu Gly Pro Arg Glu Asn Gln Asp Pro Pro Pro Arg 1085 1075 1080 Pro Leu Ala Arg His Leu Ser Asp Ala Asp Arg Leu Arg Lys Val Ile 1095 Gln Glu Leu Val Asp Thr Glu Lys Ser Tyr Val Lys Asp Leu Ser Cys 1110 1115 Leu Phe Glu Leu Tyr Leu Glu Pro Leu Gln Asn Glu Thr Phe Leu Thr 1130 1125 Gln Asp Glu Met Glu Ser Leu Phe Gly Ser Leu Pro Glu Met Leu Glu 1140 1145 1150 Phe Gln Lys Val Phe Leu Glu Thr Leu Glu Asp Gly Ile Ser Ala Ser 1160 1155 Ser Asp Phe Asn Thr Leu Glu Thr Pro Ser Gln Phe Arg Lys Leu Leu 1180 1175 Phe Ser Leu Gly Gly Ser Phe Leu Tyr Tyr Ala Asp His Phe Lys Leu 1195 1190 Tyr Ser Gly Phe Cys Ala Asn His Ile Lys Val Gln Lys Val Leu Glu 1205 1210 Arg Ala Lys Thr Asp Lys Ala Phe Lys Ala Phe Leu Asp Ala Arg Asn 1220 1225 Pro Thr Lys Gln His Ser Ser Thr Leu Glu Ser Tyr Leu Ile Lys Pro 1240 1245 Val Gln Arg Val Leu Lys Tyr Pro Leu Leu Leu Lys Glu Leu Val Ser 1250 1255 1260 Leu Thr Asp Gln Glu Ser Glu Glu His Tyr His Leu Thr Glu Ala Leu

1270 1275 Lys Ala Met Glu Lys Val Ala Ser His Ile Asn Glu Met Gln Lys Ile 1285 1290 Tyr Glu Asp Tyr Gly Thr Val Phe Asp Gln Leu Val Ala Glu Gln Ser 1305 1300 Gly Thr Glu Lys Glu Val Thr Glu Leu Ser Met Gly Glu Leu Leu Met 1325 1320 His Ser Thr Val Ser Trp Leu Asn Pro Phe Leu Ser Leu Gly Lys Ala 1335 1340 Arg Lys Asp Leu Glu Leu Thr Val Phe Val Phe Lys Arg Ala Val Ile 1350 1355 Leu Val Tyr Lys Glu Asn Cys Lys Leu Lys Lys Leu Pro Ser Asn 1365 1370 Ser Arg Pro Ala His Asn Ser Thr Asp Leu Asp Pro Phe Lys Phe Arg 1380 1385 1390 Trp Leu Ile Pro Ile Ser Ala Leu Gln Val Arg Leu Gly Asn Pro Ala 1400 1405 Gly Thr Glu Asn Asn Ser Ile Trp Glu Leu Ile His Thr Lys Ser Glu 1410 1415 1420 Ile Glu Gly Arg Pro Glu Thr Ile Phe Gln Leu Cys Cys Ser Asp Ser 1435 1430 Glu Ser Lys Thr Asn Ile Val Lys Val Ile Arg Ser Ile Leu Arg Glu 1445 1450 Asn Phe Arq Arq His Ile Lys Cys Glu Leu Pro Leu Glu Lys Thr Cys 1460 1465 1470 Lys Asp Arg Leu Val Pro Leu Lys Asn Arg Val Pro Val Ser Ala Lys 1475 1480 1485 Leu Ala Ser Ser Arg Ser Leu Lys Val Leu Lys Asn Ser Ser Ser Asn 1495 1500 Glu Trp Thr Gly Glu Thr Gly Lys Gly Thr Leu Leu Asp Ser Asp Glu 1510 1515 Gly Ser Leu Ser Ser Gly Thr Gln Ser Ser Gly Cys Pro Thr Ala Glu 1530 1525 Gly Arg Gln Asp Ser Lys Ser Thr Ser Pro Gly Lys Tyr Pro His Pro 1545 Gly Leu Ala Asp Phe Ala Asp Asn Leu Ile Lys Glu Ser Asp Ile Leu 1555 1560 1565 Ser Asp Glu Asp Asp Asp His Arg Gln Thr Val Lys Gln Gly Ser Pro 1570 1575 1580 Thr Lys Asp Ile Glu Ile Gln Phe Gln Arg Leu Arg Ile Ser Glu Asp 1590 1595 Pro Asp Val His Pro Glu Ala Glu Gln Gln Pro Gly Pro Glu Ser Gly 1610 1605 Glu Gly Gln Lys Gly Gly Glu Gln Pro Lys Leu Val Arg Gly His Phe 1620 1625 1630 Cys Pro Ile Lys Arg Lys Ala Asn Ser Thr Lys Arg Asp Arg Gly Thr 1640 Leu Leu Lys Ala Gln Ile Arg His Gln Ser Leu Asp Ser Gln Ser Glu 1660 1655 Asn Ala Thr Ile Asp Leu Asn Ser Val Leu Glu Arg Glu Phe Ser Val 1670 1675 Gln Ser Leu Thr Ser Val Val Ser Glu Glu Cys Phe Tyr Glu Thr Glu 1690 1685 Ser His Gly Lys Ser 1700

<211> 5106 <212> DNA

<213> Homo sapiens

<400> 3

atgggcaact ccgacagtca gtacaccctt caaggatcta aaaatcatag caatactatt 60 120 actggtqcta agcaaattcc ttgctccctg aaaatacgtg gcgttcatgc aaaagaggaa aagtcattgc atggatgggg tcacgggagc aacggagcag gttacaagtc caggtccctg 180 georgaaget geetttetea etttaagagt aaceageett aegeategag aeteggtgge 240 300 cccacatgca aggtctccag aggtgttgcc tactccacgc acaggacaaa tgccccaggg 360 aaggatttcc agggcatcag tgctgctttc tcaactgaga atggcttcca ttctgttggc 420 cacgagetgg cagataacca catcacetee agagaetgea aeggaeacet teteaactge 480 tacgggagga atgagagcat tgcctccacc ccaccgggcg aagaccgcaa gagcccccga 540 gtgctcatca aaacgctggg gaagccggat gggtgtttaa gggtcgagtt ccacaatggt ggcaacccca gcaaagtgcc tgcagaggac tgcagtgagc cggtgcagct gctgaggtac 600 660 tcacctacct tagcatcgga aacctcccct gtgcctgaag ccaggagggg gtccagcgcc 720 gattecetge ecagecateg eccetetece aeggaetete geetgeggte eagcaaagge 780 agctccctga gttctgagtc atcctggtac gactcccctt ggggcaatgc tggagagctg 840 agegaggetg agggeteett cetggeeece ggeatgeetg acceeagtet ceatgeeage 900 ttcccacctg gcgatgccaa aaagcctttc aaccaaagct cttccctctc ctccctccgg gaactgtaca aagatgccaa cctggggagc ctctccccct caggtatccg cctttctgat 960 gaatacatgg gcacgcatgc cagcctgagc aaccgtgtct cttttgcttc cgacattgat 1020 1080 gtgccctcca gagtggcaca cggggacccc atccagtaca gttccttcac tctcccctgt cggaagccca aagcctttgt tgaggatact gcgaagaagg actccctcaa agccaggatg 1140 1200 cqacqqatca qtqactqqac qqgaaqcctc tcaaqqaaqa aaaqqaaact ccaqqaqccq aggtccaagg agggcagtga ctactttgac agtcgctctg atggactgaa tacagatgtg 1260 1320 cagggatect eccaggeate tgettttetg tggteagggg getetactea gateetgtet cagagaagtg aatccacaca tgcgattggc agcgatcccc tccggcagaa catttatgag 1380 1440 aatttcatgc gagagttgga aatgagcagg accaacactg agaacataga aacatctaca 1500 gaaaccgccg agtccagcag cgagtcactc agctctctgg aacagctgga tctgctcttc 1560 gagaaggaac agggggtggt ccggagggcc gggtggctct tcttcaagcc cctggtcact 1620 gtgcagaagg aaaggaagct tgagctggtg gcacgaagga aatggaaaca gtactgggta 1680 acgctgaaag gatgcacgct gctgttttat gagacctatg ggaagaattc catggatcag agcagtgccc ctcggtgtgc tctgtttgca gaagacagca tagtgcagtc tgttccagag 1740 1800 catcccaaga aagaaaatgt gttctgcctc agcaactcct ttggagatgt ctaccttttc 1860 caggccacca gccagacaga tctagaaaac tgggtcactg ctgtacactc tgcttgtgca 1920 tccctttttg caaagaagca tgggaaagag gacacgctgc ggctgctgaa gaaccagacc 1980 aaaaacctgc ttcagaagat agacatggac agcaagatga agaagatggc agagctgcag ctgtccgtgg tgagcgaccc aaagaacagg aaagccatag agaaccagat ccagcaatgg 2040 2100 qaqcaqaatc ttgagaaatt tcacatggat ctgttcagga tgcgctgcta tctggccagc ctacaaggtg gggagttacc gaacccaaag agtctccttg cagccgccag ccgcccctcc 2160 2220 aagctggccc tcggcaggct gggcatcttg tctgtttcct ctttccatgc tctggtatgt tctagagatg actctgctct ccggaaaagg acactgtcac tgacccagcg agggagaaac 2280 2340 aagaagggaa tattttcttc gttaaaaggg ctggacacac tggccagaaa aggcaaggag aagagacctt ctataactca ggtcgatgaa cttctgcata tatatggttc aacagtggac 2400 2460 ggtgttcccc gagacaatgc atgggaaatc cagacttatg ttcactttca ggacaatcac ggagttactg tagggatcaa gccagagcac agagtagaag atattttgac tttggcatgc 2520 aagatgaggc agttggaacc cagccattat ggcctacagc ttcgaaaatt agtagatgac 2580 aatgttgagt attgcatccc tgcaccatat gaatatatgc aacaacaggt ttatgatgaa 2640 atagaagtct ttccactaaa tgtttatgat gtgcagctca cgaagactgg gagtgtgtgt 2700 2760 gactttgggt ttgcagttac agcgcaggtg gatgagcgtc agcatctcag ccggatattt 2820 ataagcgacg ttcttcccga tggcctggcg tatggggaag ggctgagaaa gggcaatgag 2880 atcatgacct taaatgggga agctgtgtct gatcttgacc ttaagcagat ggaggccctg ttttctgaga agagcgtcgg actcactctg attgcccggc ctccggacac aaaagcaacc 2940 3000 ctgtgtacat cctggtcaga cagtgacctg ttctccaggg accagaagag tctgctgccc 3060 cctcctaacc aqtcccaact gctggaggaa ttcctggata actttaaaaa gaatacagcc aatgatttca gcaacgtccc tgatatcaca acaggtctga aaaggagtca gacagatggc 3120 actetqqate aqqttteeca caqqqaqaaa atqqaqeaqa catteagqaq tqetqaqeaq 3180 3240 atcactqcac tqtqcaqqaq ttttaacqac agtcaggcca acggcatgga aggaccgcgg 3300 gagaatcagg atcetecte gaggeetetg geeegeeace tgtetgatge agacegeete cgcaaagtca tccaggagct tgtggacaca gagaagtcct acgtgaagga tttgagctgc 3360 ctctttqaat tatacttqqa qccacttcaq aatqaqacct ttcttaccca agatqaqatq 3420 3480 gagtcacttt ttggaagttt gccagagatg cttgagtttc agaaggtgtt tctggagacc 3540 ctggaggatg ggatttcagc atcatctgac tttaacaccc tagaaacccc ctcacagttt agaaaattac tgttttccct tggaggctct ttcctttatt acgcggacca ctttaaactg 3600 tacagtggat tctgtgctaa ccatatcaaa gtacagaagg ttctggagcg agctaaaact 3660 3720 qacaaaqcct tcaaggcttt tctggatgcc cggaacccca ccaagcagca ttcctccacg 3780 ctggagtect accteateaa geeggtteag agagtgetea agtaceeget getgeteaag gagctggtgt ccctgacgga ccaggagagc gaggagcact accacctgac ggaagcacta 3840 3900 aaggcaatgg agaaagtagc gagccacatc aatgagatgc agaagatcta tgaggattat 3960 gggaccgtgt ttgaccagct agtagctgag cagagcggaa cagagaagga ggtaacagaa 4020 ctttcqatqq qaqaqcttct qatqcactct acggtttcct ggttgaatcc atttctgtct ctaggaaaag ctagaaagga ccttgagctc acagtatttg tttttaagag agccgtcata 4080 ctqqtttata aaqaaaactg caaactgaaa aagaaattgc cctcgaattc ccggcctgca 4140 4200 cacaactcta ctgacttgga cccatttaaa ttccgctggt tgatccccat ctccgcgctt caagtcagac tggggaatcc agcagggaca gaaaataatt ccatatggga actgatccat 4260 acgaagtcag aaatagaagg acggccagaa accatctttc agttgtgttg cagtgacagt 4320 qaaaqcaaaa ccaacattqt taaggtgatt cgttctattc tgagggaaaa cttcaggcgt 4380 4440 cacataaagt gtgaattacc actggagaaa acgtgtaagg atcgcctggt acctcttaag 4500 aaccgagttc ctgtttcggc caaattagct tcatccaggt ctttaaaagt cctgaagaat 4560 tectecagea acgagtggae eggtgagaet ggeaagggaa eettgetgga etetgaegag ggcagcttga gcagcggcac ccagagcagc ggctgcccca cggctgaggg caggcaggac 4620 4680 tocaaqaqca cttctcccqq qaaataccca caccccqqct tqqcaqattt tqccqacaat ctcatcaaag agagtgacat cctgagcgat gaagatgatg accaccgtca gactgtgaag 4740 cagggcagcc ctactaaaga catcgaaatt cagttccaga gactgaggat ttccgaggac 4800 4860 ccaqacqttc accccqaqqc tgagcagcag cctggcccgg agtcgggtga gggtcagaaa ggaggagagc agcccaaact ggtccggggg cacttctgcc ccattaaacg aaaagccaac 4920 4980 agcaccaaga gggacagagg aactttgctc aaggcgcaga tccgtcacca gtcccttgac agtcagtctg aaaatgccac catcgaccta aattctgttc tagagcgaga attcagtgtc 5040 5100 caqaqtttaa catctqttqt cagtgaggag tgtttttatg aaacagagag ccacggaaaa 5106 tcatag

```
<210> 4
<211> 85
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<400> 4
Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys
                                     10
                                                         15
Arg Tyr Phe Val Leu Phe Asn Asn Val Leu Leu Tyr Tyr Lys Asp Ser
                                 25
Lys Lys Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Gln Val Glu
                             40
Lys Pro Asp Lys Asn Cys Phe Glu Ile Arg Thr Asp Arg Thr Leu Leu
                         55
Leu Gln Ala Glu Ser Glu Glu Glu Arg Lys Glu Trp Val Lys Ala Ile
                                         75
                    70
Gln Ser Ala Ile Arg
```

<210> 5 <211> 77 <212> PRT <213> Artificial Sequence <220> <223> Consensus sequence <400> 5 Lys Thr Ile Arg Val His Leu Pro Asn Asn Gln Arg Ser Val Val Glu 1 Val Arg Pro Gly Met Thr Val Arg Asp Ala Leu Ala Lys Ala Leu Lys Lys Arg Gly Leu Asn Pro Ser Ala Cys Val Val Arg Arg Ser Gly Asp 40 45 Pro Gln Glu Gly Glu Lys Lys Pro Leu Asp Leu Asp Thr Asp Ile Ser Ser Leu Pro Gly Pro Glu Glu Leu Val Val Glu Asn Leu 70 <210> 6 <211> 83 <212> PRT <213> Artificial Sequence <220> <223> Consensus sequence <400> 6 Glu Ile Thr Leu Glu Lys Glu Val Lys Arg Gly Gly Leu Gly Phe Ser Ile Lys Gly Gly Ser Asp Lys Gly Ile Val Val Ser Glu Val Leu Pro 25 Gly Ser Gly Ala Ala Glu Ala Gly Gly Arg Leu Lys Glu Gly Asp Val 40 Ile Leu Ser Val Asn Gly Gln Asp Val Glu Asn Met Ser His Glu Arg 55 Ala Val Leu Ala Ile Lys Gly Ser Gly Gly Glu Val Thr Leu Thr Val 70 Leu Arg Asp <210> 7 <211> 207 <212> PRT <213> Artificial Sequence <220> <223> Consensus sequence <400> 7 Val Leu Lys Glu Leu Leu Glu Thr Glu Lys Lys Tyr Val Arg Asp Leu 10 Glu Ile Leu Asp Asn Val Tyr Met Lys Pro Leu Arg Glu Ala Ala Ile 25 20

Ser Ser Lys Pro Val Leu Thr Pro Asp Asp Ile Glu Thr Ile Phe Ser 40 35 Asn Ile Glu Asp Ile Tyr Glu Phe His Arg Glu Phe Leu Lys Ser Ser Leu Glu Ala Arg Ile Ser Ser Ser Gln Phe Glu Asp Leu Asp Glu Lys 70 75 Lys Ile Glu Pro Ser Ala Pro Arg Leu Gly Asp Leu Phe Leu Lys Leu 90 Lys Glu Pro Phe Leu Gln Val Tyr Gly Glu Tyr Cys Ser Asn Lys Pro 105 100 Tyr Ala Gln Glu Leu Leu Glu Lys Leu Arg Gln Ala Ala Ser Asn Pro 120 Gln Phe Ala Glu Phe Leu Asp Glu Val Glu Ala Ser Ser Asn Thr Gly 140 135 Ala Lys Asp Asp Ala Val Lys Leu Thr Leu Gln Ser Leu Leu Lys 150 155 Pro Val Gln Arg Ile Leu Arg Tyr Pro Leu Leu Leu Lys Glu Leu Leu 170 Lys His Thr Pro Glu Gly Glu Asp Gln Pro Asp Arg Glu Asp Leu Lys 185 180 Lys Ala Leu Asp Leu Leu Gln Asp Leu Ala Lys Ser Ile Asn Glu 200 <210> 8 <211> 67 <212> PRT <213> Artificial Sequence <223> Consensus sequence <400> 8 Phe Val Leu Phe Asn Asn Val Leu Leu Tyr Tyr Lys Asp Ser Lys Lys 10 Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Gln Val Glu Lys Pro 25 Asp Lys Asn Cys Phe Glu Ile Arg Thr Asp Arg Thr Leu Leu Leu Gln 40 Ala Glu Ser Glu Glu Glu Arg Lys Glu Trp Val Lys Ala Ile Gln Ser 55 Ala Ile Arg 65 <210> 9 <211> 82 <212> PRT <213> Artificial Sequence <220> <223> Consensus sequence <400> 9 Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys 10 Arg Tyr Phe Val Leu Phe Asn Gly Val Leu Leu Tyr Tyr Lys Ser Lys 25 Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Ser Val Arg Glu Pro

```
THULLIST HUBEL
```

```
45
                            40
Cys Phe Glu Ile Val Thr Asp Arg Thr Leu Leu Gln Ala Glu Ser
                       55
Glu Glu Glu Arg Glu Glu Trp Val Glu Ala Leu Gln Ser Ala Ile Ala
                    70
Lys Ala
<210> 10
<211> 76
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<400> 10
Lys Thr Cys Arg Val His Leu Pro Asp Asn Gln Arg Thr Val Val Lys
                                   10
Val Arg Pro Gly Lys Thr Val Arg Asp Ala Leu Ala Lys Ala Leu Lys
Lys Arg Gly Leu Asn Pro Glu Ala Cys Val Val Arg Leu Arg Gly Asp
                            40
Pro Gln Glu Gly Glu Lys Lys Pro Leu Asp Leu Asn Gln Asp Ile Ser
                        55
Ser Leu Ala Gly Gln Glu Leu Val Val Glu Glu Leu
<210> 11
<211> 80
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
Gly Gly Leu Gly Phe Ser Ile Val Gly Gly Ile Phe Val Ser Ser Val
                                     10 -
Val Pro Gly Ser Pro Ala Ala Lys Ala Gly Arg Lys Ser Leu Gly Leu
                                 25
Leu Lys Val Gly Asp Val Ile Leu Glu Val Asn Gly Glu Thr Ser Val
                             40
Glu Gly Leu Thr His Glu Glu Ala Val Asp Leu Leu Lys Lys Ala Gly
Gly Gly Gly Val Gly Glu Lys Val Thr Leu Thr Val Leu Arg Gly Gly
<210> 12
<211> 211
<212> PRT
<213> Artificial Sequence
<220>
<223> Consensus sequence
<400> 12
```

Lys Ala

Val Leu Lys Glu Leu Leu Gln Thr Glu Arg Asn Tyr Val Arg Asp Leu 5 10 Lys Ile Leu Val Glu Val Phe Leu Lys Pro Leu Lys Lys Glu Ala Lys Ser Ser Leu Leu Pro Leu Leu Ser Pro Asp Glu Val Lys Thr Leu Phe 40 Gly Pro Asn Ile Glu Glu Ile Tyr Glu Phe His Arg Arg Phe Leu Asp 55 Glu Leu Glu Glu Arg Val Glu Glu Trp Leu Leu Ser Lys Asp Leu Lys 7.5 70 Ser Glu Arg Asn Ser Val Ile Glu Asp Ser Gly Glu Arg Ile Gly Asp 90 Val Phe Leu Lys Leu Phe Ser Ala Glu Glu Phe Phe Lys Ile Tyr Ser 105 100 Glu Tyr Cys Ser Asn His Pro Asp Ala Leu Glu Leu Leu Lys Lys Leu 120 Met Lys Lys Lys Asn Pro Ala Phe Gln Lys Phe Leu Lys Glu Ile 140 135 Glu Ser Lys Pro Asn Cys Arg Ser Lys Ser Glu Ala Arg Leu Thr Leu 155 150 Glu Ser Leu Leu Ile Lys Pro Val Gln Arg Leu Thr Lys Tyr Pro Leu 170 165 Leu Leu Lys Glu Leu Leu Lys His Thr Pro Pro Asp His Glu Asp Arg 185 180 Glu Asp Leu Lys Lys Ala Leu Glu Ala Ile Lys Glu Leu Ala Ser Gln 200 Val Asn Glu 210 <210> 13 <211> 82 <212> PRT <213> Artificial Sequence <220> <223> Consensus sequence <400> 13 Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Lys Ser Trp Lys Lys Arg Tyr Phe Val Leu Phe Asn Gly Val Leu Leu Tyr Tyr Lys Ser Lys 25 Lys Pro Lys Gly Ser Ile Pro Leu Ser Gly Cys Ser Val Arg Glu Pro 40 Cys Phe Glu Ile Val Thr Asp Arg Thr Leu Leu Leu Gln Ala Glu Ser Glu Glu Glu Arg Glu Glu Trp Val Glu Ala Leu Gln Ser Ala Ile Ala